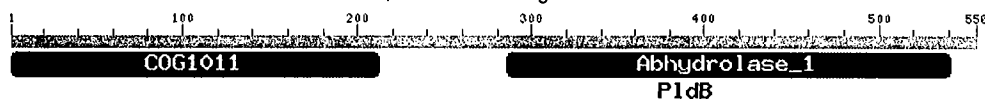


**BLAST Basic Local Alignment Search Tool**Job Title: human soluble epoxide hydrolase BLAST

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Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.

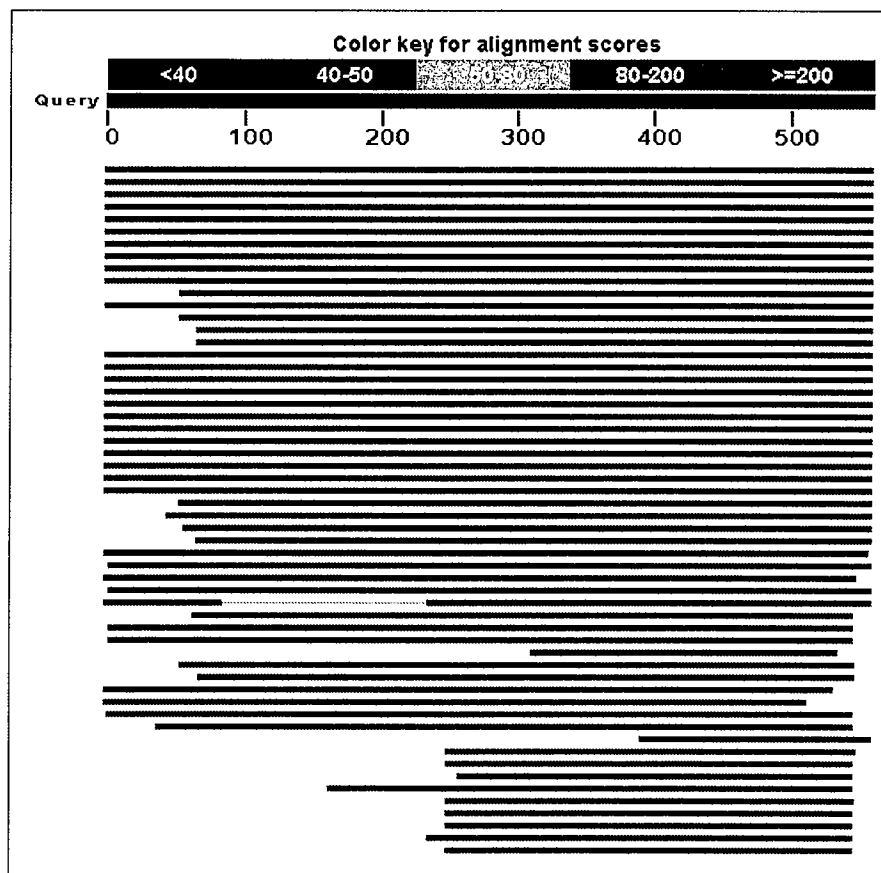
**BLASTP 2.2.18 (Mar-02-2008)**

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402. Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109. RID: 19UBW5CM014 Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects 6,470,629 sequences; 2,208,486,882 total letters

Query= Length=556

**Distribution of 101 Blast Hits on the Query Sequence**

---



Distance tree of results **NEW**

Score

**E**

Sequences producing significant alignments:

(Bits) Value

|                                                                            |      |        |           |
|----------------------------------------------------------------------------|------|--------|-----------|
| gb AA014968.1 AF033336_1 soluble epoxide hydrolase [Homo sapi...           | 1157 | 0.0    | <b>G</b>  |
| gb AA014968.1 AF033336_1 Homo sapiens epoxide hydrolase 2, cytoplasmic ... | 1151 | 0.0    |           |
| ref NP_001070.2  epoxide hydrolase 2, cytoplasmic [Homo sapie...           | 1150 | 0.0    | <b>UG</b> |
| gb AA014967.1 AF233335_1 soluble epoxide hydrolase [Homo sapi...           | 1149 | 0.0    | <b>G</b>  |
| ref XP_001163779.1  PREDICTED: epoxide hydrolase 2, cytoplasm...           | 1141 | 0.0    | <b>UG</b> |
| gb EAW63547.1  epoxide hydrolase 2, cytoplasmic, isoform CRA_...           | 1140 | 0.0    | <b>G</b>  |
| gb AAA02756.1  cytosolic epoxide hydrolase                                 | 1139 | 0.0    | <b>G</b>  |
| ref XP_001163855.1  PREDICTED: epoxide hydrolase 2, cytoplasm...           | 1126 | 0.0    | <b>G</b>  |
| ref XP_001099474.1  PREDICTED: similar to epoxide hydrolase 2...           | 1083 | 0.0    | <b>UG</b> |
| ref XP_001163855.1  PREDICTED: epoxide hydrolase 2, cytoplasm...           | 1076 | 0.0    | <b>G</b>  |
| gb EAW63547.1  epoxide hydrolase 2, cytoplasmic, isoform CRA_...           | 1045 | 0.0    | <b>G</b>  |
| ref XP_001163779.1  PREDICTED: epoxide hydrolase 2, cytoplasm...           | 1040 | 0.0    | <b>UG</b> |
| ref XP_001163857.1  PREDICTED: epoxide hydrolase 2, cytoplasm...           | 1036 | 0.0    | <b>UG</b> |
| gb EAW63551.1  epoxide hydrolase 2, cytoplasmic, isoform CRA_...           | 1019 | 0.0    | <b>G</b>  |
| ref XP_001163855.1  PREDICTED: epoxide hydrolase 2, cytoplasm...           | 1011 | 0.0    | <b>UG</b> |
| ref XP_534560.1  PREDICTED: similar to epoxide hydrolase 2, c...           | 931  | 0.0    | <b>UG</b> |
| ref XP_857471.1  PREDICTED: similar to epoxide hydrolase 2, c...           | 930  | 0.0    | <b>UG</b> |
| ref XP_001402725.1  PREDICTED: similar to soluble epoxide hyd...           | 929  | 0.0    | <b>UG</b> |
| ref NP_001001641.1  soluble epoxide hydrolase [Sus scrofa] >s...           | 924  | 0.0    | <b>UG</b> |
| ref XP_857554.1  PREDICTED: similar to epoxide hydrolase 2, c...           | 919  | 0.0    | <b>UG</b> |
| ref XP_857430.1  PREDICTED: similar to epoxide hydrolase 2, c...           | 912  | 0.0    | <b>UG</b> |
| ref NP_001069002.1  epoxide hydrolase 2, cytoplasmic [Bos tau...           | 902  | 0.0    | <b>UG</b> |
| emb CAA85471.1  Epoxide Hydrolase [Mus musculus]                           | 877  | 0.0    | <b>G</b>  |
| ref NP_031966.2  epoxide hydrolase 2, cytoplasmic [Mus muscul...           | 875  | 0.0    | <b>UG</b> |
| dbj BAE25172.1  unnamed protein product [Mus musculus]                     | 874  | 0.0    | <b>G</b>  |
| ref NP_076225.1  epoxide hydrolase 2, cytoplasmic [Rattus nor...           | 870  | 0.0    | <b>UG</b> |
| gb AAH89732.1  Epoxide hydrolase 2, cytoplasmic [Rattus norve...           | 865  | 0.0    | <b>G</b>  |
| gb E0136006.1  epoxide hydrolase 2, cytoplasmic, isoform CRA_...           | 814  | 0.0    | <b>G</b>  |
| gb E0136377.1  epoxide hydrolase 2, cytoplasmic, isoform CRA_...           | 811  | 0.0    | <b>G</b>  |
| gb AAM28338.1  ovary-selective epoxide hydrolase [Mus musculus]            | 803  | 0.0    | <b>G</b>  |
| gb ABU95055.1  epoxide hydrolase 2C [Mus musculus]                         | 791  | 0.0    | <b>G</b>  |
| ref XP_001330051.1  PREDICTED: similar to soluble epoxide hyd...           | 717  | 0.0    | <b>UG</b> |
| ref NP_001096912.1  epoxide hydrolase 2, cytoplasmic [Xenopus...           | 677  | 0.0    | <b>UG</b> |
| ref NP_001096917.1  epoxide hydrolase 2, cytoplasmic [Gallus ...           | 675  | 0.0    | <b>UG</b> |
| ref NP_001097147.1  epoxide hydrolase 2, cytoplasmic [Xenopus...           | 669  | 0.0    | <b>UG</b> |
| emb CAH91370.1  hypothetical protein [Pongo pygmaeus]                      | 644  | 0.0    |           |
| ref XP_001521600.1  PREDICTED: similar to epoxide hydrolase 2...           | 612  | 3e-173 | <b>UG</b> |
| ref NP_001098642.1  epoxide hydrolase 2, cytoplasmic [Danio r...           | 572  | 2e-161 | <b>UG</b> |
| emb CAG00866.1  unnamed protein product [Tetraodon nigroviridis]           | 479  | 4e-133 |           |
| gb EAW63550.1  epoxide hydrolase 2, cytoplasmic, isoform CRA_...           | 463  | 1e-128 | <b>G</b>  |
| ref XP_725168.2  PREDICTED: similar to Ephx2-prov protein [St...           | 454  | 8e-126 | <b>UG</b> |
| ref XP_001164789.1  PREDICTED: similar to Ephx2-prov protein ...           | 448  | 3e-124 | <b>UG</b> |
| ref XP_001190554.1  PREDICTED: similar to Ephx2-prov protein ...           | 420  | 1e-115 | <b>UG</b> |
| ref XP_725076.2  PREDICTED: similar to Ephx2-prov protein, pa...           | 420  | 2e-115 | <b>UG</b> |
| ref XP_001641873.1  predicted protein [Nematostella vectensis...           | 404  | 1e-110 | <b>G</b>  |
| ref XP_001191957.1  PREDICTED: similar to soluble epoxide hyd...           | 309  | 4e-82  | <b>UG</b> |
| ref XP_001253507.1  PREDICTED: hypothetical protein [Bos taurus]           | 284  | 1e-74  | <b>UG</b> |
| ref NP_767754.1  epoxide hydrolase [Bradyrhizobium japonicum ...           | 236  | 4e-60  | <b>G</b>  |
| ref YP_486290.1  Alpha/beta hydrolase [Rhodopseudomonas palus...           | 235  | 6e-60  | <b>G</b>  |
| ref YP_001413763.1  alpha/beta hydrolase fold [Parvibaculum l...           | 234  | 1e-59  | <b>G</b>  |
| ref XP_001179641.1  PREDICTED: similar to soluble epoxide hyd...           | 234  | 1e-59  | <b>UG</b> |
| ref NP_120043.1  epoxide hydrolase [Caulobacter crescentus CB...           | 232  | 5e-59  | <b>G</b>  |
| ref XP_001683329.1  alpha/beta hydrolase fold [Caulobacter sp...           | 231  | 1e-58  | <b>G</b>  |
| ref YP_761108.1  putative epoxide hydrolase [Hyphomonas neptu...           | 227  | 2e-57  | <b>G</b>  |
| ref NP_821315.1  epoxide hydrolase [Streptomyces avermitilis ...           | 223  | 3e-56  | <b>G</b>  |
| ref YP_562843.1  alpha/beta hydrolase fold [Rhodopseudomonas ...           | 223  | 4e-56  | <b>G</b>  |

|                    |                                                   |     |       |   |
|--------------------|---------------------------------------------------|-----|-------|---|
| gb E0147179.1      | epoxide hydrolase 2, cytoplasmic, isoform CRA_... | 204 | 4e-56 | G |
| ref NP_219174.1    | PROBABLE EPOXIDE HYDROLASE EPHA (EPOXIDE HYD...   | 204 | 7e-56 | G |
| ref YP_001210928.1 | alpha/beta hydrolase fold [Clostridium be...      | 219 | 3e-55 | G |
| ref YP_001853477.1 | epoxide hydrolase Epha [Mycobacterium mar...      | 218 | 8e-55 | G |
| ref YP_007699.1    | epoxide hydrolase Epha [Mycobacterium ulcera...   | 218 | 8e-55 | G |
| ref NP_771160.1    | epoxide hydrolase [Bradyrhizobium japonicum ...   | 218 | 1e-54 | G |
| ref YP_029896.1    | putative epoxide hydrolase [Myxococcus xanth...   | 217 | 2e-54 | G |
| ref NP_959380.1    | Epha [Mycobacterium avium subsp. paratubercu...   | 217 | 2e-54 | G |
| ref ZF_00877473.1  | COG0596: Predicted hydrolases or acyltrans...     | 216 | 3e-54 |   |
| ref ZF_02299340.1  | alpha/beta hydrolase fold [Rhodopseudomona...     | 216 | 4e-54 |   |
| ref NP_354796.1    | epoxide hydrolase [Agrobacterium tumefaciens...   | 216 | 5e-54 | G |
| ref YP_079919.1    | hydrolase, alpha/beta fold family protein (M...   | 215 | 6e-54 | G |
| ref NP_027771.1    | epoxide hydrolase [Streptomyces coelicolor A...   | 215 | 9e-54 | G |
| ref YP_001701281.1 | Probable epoxide hydrolase Epha [Mycobact...      | 214 | 1e-53 | G |
| ref YP_001240076.1 | Putative epoxide hydrolase [Bradyrhizobiu...      | 214 | 1e-53 | G |
| ref NP_949116.1    | epoxide hydrolase [Rhodopseudomonas palustri...   | 214 | 2e-53 | G |
| ref YP_001238693.1 | putative epoxide hydrolase [Bradyrhizobiu...      | 213 | 3e-53 | G |
| ref NP_326951.2    | epoxide hydrolase [Agrobacterium tumefaciens...   | 213 | 4e-53 | G |
| emb CAC44404.1     | putative epoxide hydrolase [Streptomyces rimo...  | 209 | 3e-52 |   |
| ref ZF_01864412.1  | putative epoxide hydrolase [Erythrobacter ...     | 209 | 4e-52 |   |
| ref YP_001244572.1 | putative epoxide hydrolase [Bradyrhizobiu...      | 209 | 4e-52 | G |
| ref ZF_01712897.1  | probable epha protein-Mycobacterium tuberc...     | 209 | 6e-52 |   |
| ref YP_569556.1    | alpha/beta hydrolase fold [Rhodopseudomonas ...   | 204 | 2e-50 | G |
| gb ABK21215.1      | unknown [Picea sitchensis]                        | 202 | 3e-50 |   |
| ref NP_769521.1    | epoxide hydrolase [Bradyrhizobium japonicum ...   | 202 | 6e-50 | G |
| emb CAC44314.1     | unnamed protein product [Vitis vinifera]          | 201 | 9e-50 |   |
| ref ZF_01507828.1  | alpha/beta hydrolase fold [Burkholderia ph...     | 200 | 2e-49 |   |
| ref ZF_01616404.1  | epoxide hydrolase [marine gamma proteobact...     | 200 | 2e-49 |   |
| ref YP_652156.1    | hydrolase, alpha/beta fold family [Alcanivor...   | 199 | 4e-49 | G |
| ref YP_791780.1    | alpha/beta hydrolase fold [Rhodopseudomonas ...   | 199 | 4e-49 | G |
| ref YP_260035.1    | epha [Pseudomonas fluorescens Pf-5] >gb AAY9...   | 199 | 5e-49 | G |
| ref YP_001205815.1 | epoxide hydrolase [Bradyrhizobium sp. ORS...      | 199 | 6e-49 | G |
| gb ABL97491.1      | putative epoxide hydrolase [uncultured marine ... | 199 | 7e-49 |   |
| ref NP_824987.1    | epoxide hydrolase [Streptomyces avermitilis ...   | 199 | 7e-49 | G |
| ref YE_703564.1    | probable epoxide hydrolase [Rhodococcus sp. ...   | 199 | 9e-49 | G |
| ref YP_890327.1    | epoxide hydrolase [Mycobacterium smegmatis s...   | 198 | 1e-48 | G |
| dbj BAD13534.1     | soluble epoxide hydrolase [Citrus jambhiri]       | 199 | 1e-48 |   |
| ref NP_823081.1    | epoxide hydrolase [Streptomyces avermitilis ...   | 197 | 1e-48 | G |
| ref YP_00107110.1  | alpha/beta hydrolase fold [Mycobacterium ...      | 197 | 2e-48 | G |
| ref NP_014921.1    | alpha/beta hydrolase fold [Caulobacter sp...      | 196 | 3e-48 | G |
| ref YP_041941.1    | alpha/beta hydrolase fold [Mycobacterium sp....   | 196 | 4e-48 | G |
| prf 11802377A      | epoxide hydrolase                                 | 195 | 8e-48 |   |
| gb ABN08020.1      | Epoxide hydrolase [Medicago truncatula]           | 194 | 2e-47 |   |
| gb ABL97724.1      | epoxide hydrolase [uncultured marine bacterium... | 194 | 2e-47 |   |

## Alignments

```

>gb|AAG14968.1|AF233336_1 G soluble epoxide hydrolase [Homo sapiens]
Length=556

  GENE ID: 2053 EPHX2 | epoxide hydrolase 2, cytoplasmic [Homo sapiens]
(Over 10 PubMed links)

Score = 1157 bits (2994), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 556/556 (100%), Positives = 556/556 (100%), Gaps = 0/556 (0%)

Query 1  MTLRAAVFDLDGVLALPAVFGVLGRTEELALPRGLLNDAFQKGGPEGATTRLMKGEITL 60
Sbjct 1  MTLRAAVFDLDGVLALPAVFGVLGRTEELALPRGLLNDAFQKGGPEGATTRLMKGEITL 60

Query 61  SQWIPLMEENCRKCSETAKVCLPKNFSEIKEIFDKAISARKINRPMLQAALMLRKKGFTTA 120
Sbjct 61  SQWIPLMEENCRKCSETAKVCLPKNFSEIKEIFDKAISARKINRPMLQAALMLRKKGFTTA 120

Query 121  ILTNTWLDDRAERDGLAQLMCELKMHFDLIESCQVGMVKPEPQIYKFLDLTLKASPSEV 180
Sbjct 121  ILTNTWLDDRAERDGLAQLMCELKMHFDLIESCQVGMVKPEPQIYKFLDLTLKASPSEV 180

Query 181  VFLDDIGANLKPARDLGMVTILVQDPTDALKLEKVTGIQLLNTAPAPLPTSCNPDSMSHG 240
Sbjct 181  VFLDDIGANLKPARDLGMVTILVQDPTDALKLEKVTGIQLLNTAPAPLPTSCNPDSMSHG 240

```



## Conserved Domains



NewSearch

PubMed

Nucleotide

Protein

## Structure

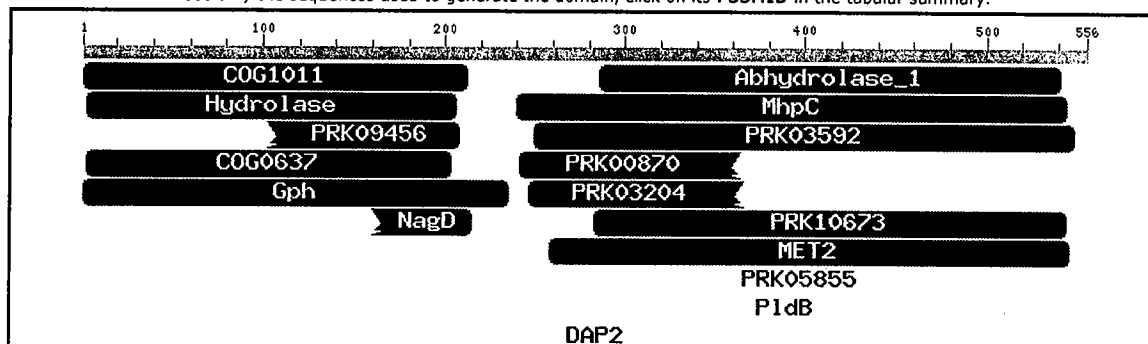
## Taxonomy

Help

**Query sequence:** [(local sequence)lcl|18838]

☐ Concise Result ☒ Full Result ☐ Show Search Information ☐

Click on the **colored bar** for a conserved domain to **view your query sequence** within the multiple sequence alignment for that domain. To see only the sequences used to generate the domain, click on its **PSSMID** in the tabular summary.



## Descriptions

|   | Title                                                                                       | Pssmid | Multi-Dom | E-value |
|---|---------------------------------------------------------------------------------------------|--------|-----------|---------|
| → | [+pfam00561, Abhydrolase_1, alpha/beta hydrolase fold. This catalytic domain is found in... | 84863  | No        | 2e-34   |
|   | [+COG0596, MhpC, Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfam... | 30941  | No        | 4e-27   |
|   | [+PRK03592, PRK03592, haloalkane dehalogenase.                                              | 81168  | No        | 8e-25   |
|   | [+PRK00870, PRK00870, haloalkane dehalogenase.                                              | 80766  | No        | 2e-18   |
| → | [+COG1011, COG1011, Predicted hydrolase (HAD superfamily) [General function prediction o... | 31215  | No        | 2e-14   |
|   | [+pfam00702, Hydrolase, haloacid dehalogenase-like hydrolase. This family are structural... | 84963  | No        | 2e-13   |
|   | [+PRK03204, PRK03204, haloalkane dehalogenase.                                              | 81112  | No        | 4e-13   |
|   | [+PRK09456, PRK09456, phosphatase.                                                          | 83014  | No        | 3e-11   |
|   | [+PRK10673, PRK10673, hypothetical protein.                                                 | 83396  | No        | 2e-07   |
|   | [+COG0637, COG0637, Predicted phosphatase/phosphohexomutase [General function prediction... | 30982  | No        | 2e-07   |
|   | [+COG0546, Gph, Predicted phosphatases [General function prediction only].                  | 30892  | No        | 5e-06   |
|   | [+COG2021, MET2, Homoserine acetyltransferase [Amino acid transport and metabolism].        | 32204  | No        | 8e-05   |
|   | [+COG0647, NagD, Predicted sugar phosphatases of the HAD superfamily [Carbohydrate trans... | 30992  | No        | 0.001   |
|   | [+PRK05855, PRK05855, short chain dehydrogenase.                                            | 81768  | Yes       | 1e-17   |
|   | [+COG2267, PldB, Lysophospholipase [Lipid metabolism].                                      | 32448  | Yes       | 1e-08   |
|   | [+COG1506, DAP2, Dipeptidyl aminopeptidases/acylaminoacyl-peptidases [Amino acid transpo... | 31695  | Yes       | 5e-05   |

## Search for similar domain architectures

**CD Search Reference:**

- <sup>11</sup> Marchler-Bauer A, Bryant SH (2004), "CD-Search: protein domain annotations on the fly.", **Nucleic Acids Res.**32(W)327-331.

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